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RAW SEQUENCE LISTING   DATE: 04/11/2002
PATENT APPLICATION: US/10/044,622   TIME: 09:14:18

Input Set : N:\Crf3\RULE60\10044622.raw
Output Set: N:\CRF3\04112002\J044622.raw

SEQUENCE LISTING

ENTERED

```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Bandman, Olga
 6                      Goli, Surya K.
 7                      Murry, Lynn E.
 9      (ii) TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
10                               FACTOR
12     (iii) NUMBER OF SEQUENCES: 3
14      (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16           (B) STREET: 3174 Porter Drive
17           (C) CITY: Palo Alto
18           (D) STATE: CA
19           (E) COUNTRY: USA
20           (F) ZIP: 94304
22       (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Diskette
24           (B) COMPUTER: IBM Compatible
25           (C) OPERATING SYSTEM: DOS
26           (D) SOFTWARE: FastSEQ for Windows Version 2.0
28      (vi) CURRENT APPLICATION DATA:
C--> 29      (A) APPLICATION NUMBER: US/10/044,622
C--> 30      (B) FILING DATE: 09-Jan-2002
31           (C) CLASSIFICATION:
33     (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: 08/788,812
35           (B) FILING DATE:
37    (viii) ATTORNEY/AGENT INFORMATION:
38           (A) NAME: Billings, Lucy J.
39           (B) REGISTRATION NUMBER: 36,749
40           (C) REFERENCE/DOCKET NUMBER: PF-0185 US
42      (ix) TELECOMMUNICATION INFORMATION:
43           (A) TELEPHONE: 415-855-0555
44           (B) TELEFAX: 415-845-4166
46 (2) INFORMATION FOR SEQ ID NO: 1:
48       (i) SEQUENCE CHARACTERISTICS:
49           (A) LENGTH: 280 amino acids
50           (B) TYPE: amino acid
51           (C) STRANDEDNESS: single
52           (D) TOPOLOGY: linear
54     (vii) IMMEDIATE SOURCE:
55           (A) LIBRARY: LUNGAST01
56           (B) CLONE: 873352
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```
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60   Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
61   1               5               10              15
62   Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
63           20              25              30
64   Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
65           35              40              45
66   Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
67       50              55              60
68   Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
69   65              70              75              80
70   Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
71               85              90              95
72   Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
73               100             105             110
74   Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
75           115             120             125
76   Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
77           130             135             140
78   Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
79   145             150             155             160
80   Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
81               165             170             175
82   Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
83               180             185             190
84   Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
85           195             200             205
86   Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
87       210             215             220
88   Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
89   225             230             235             240
90   Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
91               245             250             255
92   Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
93               260             265             270
94   Cys Lys Thr Pro Cys Pro Lys Ile
95               275             280
97 (2) INFORMATION FOR SEQ ID NO: 2:
99      (i) SEQUENCE CHARACTERISTICS:
100             (A) LENGTH: 1337 base pairs
101             (B) TYPE: nucleic acid
102             (C) STRANDEDNESS: single
103             (D) TOPOLOGY: linear
105     (vii) IMMEDIATE SOURCE:
106             (A) LIBRARY: LUNGAST01
107             (B) CLONE: 873352
109     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
111   CTGTAATAGG AGCAGTATAG GGAAACCTGG TACCCTGCAG GTACTGGTCC GGAGTTCCTG      60
112   GGTCGACCCA CGCGTCCGGC TTTCTGTAGC TGTAACATTG GTGGCCACAC ACCTCCTTAC     120
```

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```
113  AAAGCAACTA GAACCTGCGG CATACATTGG AGAGATTTTT TTAATTTTCT GGACATGAAG   180
114  TAAATTTAGA GTGCTTTCTA ATTTCAGGTA GAAGACATGT CCACCTTCTG ATTATTTTTG   240
115  GAGAACATTT TGATTTTTTT CATCTCTCTC TCCCCACCCC TAAGATTGTG CAAAAAAAGC   300
116  GTACCTTGCC TAATTGAAAT AATTTCATTG GATTTGATC AGAACTGATT ATTTGGTTTT   360
117  CTGTGTGAAG TTTTGAGGTT TCAAACTTTC CTTCTGGAGA ATGCCTTTTG AAACAATTTT   420
118  CTCTAGCTGC CTGATGTCAA CTGCTTAGTA ATCAGTGGAT ATTGAAATAT TCAAAATGTA   480
119  CAGAGAGTGG GTAGTGGTGA ATGTTTTCAT GATGTTGTAC GTCCAGCTGG TGCAGGGCTC   540
120  CAGTAATGAA CATGGACCAG TGAAGCGATC ATCTCAGTCC ACATTGGAAC GATCTGAACA   600
121  GCAGATCAGG GCTGCTTCTA GTTTGGAGGA ACTACTTCGA ATTACTCACT CTGAGGACTG   660
122  GAAGCTGTGG AGATGCAGGC TGAGGCTCAA AAGTTTTACC AGTATGGACT CTCGCTCAGC   720
123  ATCCCATCGG TCCACTAGGT TTGCGGCAAC TTTCTATGAC ATTGAAACAC TAAAAGTTAT   780
124  AGATGAAGAA TGGCAAAGAA CTCAGTGCAG CCCTAGAGAA ACGTGCGTGG AGGTGGCCAG   840
125  TGAGCTGGGG AAGAGTACCA ACACATTCTT CAAGCCCCCT TGTGTGAACG TGTTCCGATG   900
126  TGGTGGCTGT TGCAATGAAG AGAGCCTTAT CTGTATGAAC ACCAGCACCT CGTACATTTC   960
127  CAAACAGCTC TTTGAGATAT CAGTGCCTTT GACATCAGTA CCTGAATTAG TGCCTGTTAA  1020
128  AGTTGCCAAT CATACAGGTT GTAAGTGCTT GCCAACAGCC CCCGCCATC CATACTCAAT  1080
129  TATCAGAAGA TCCATCCAGA TCCCTGAAGA AGATCGCTGT TCCCATTCCA AGAAACTCTG  1140
130  TCCTATTGAC ATGCTATGGG ATAGCAACAA ATGTAAATGT GTTTTGCAGG AGGAAAATCC  1200
131  ACTTGCTGGA ACAGAAGACC ACTCTCATCT CCAGGAACCA GCTCTCTGTG GGCCACACAT  1260
132  GATGTTTGAC GAAGATCGTT GCGAGTGTGT CTGTAAAACA CCATGTCCCA AGATCTAATC  1320
133  CAGCACCCCA AAAAATG                                                 1337
135  (2) INFORMATION FOR SEQ ID NO: 3:
137      (i) SEQUENCE CHARACTERISTICS:
138            (A) LENGTH: 419 amino acids
139            (B) TYPE: amino acid
140            (C) STRANDEDNESS: single
141            (D) TOPOLOGY: linear
143     (vii) IMMEDIATE SOURCE:
144            (A) LIBRARY: GenBank
145            (B) CLONE: 1150989
147      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
149  Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
150   1               5                  10                  15
151  Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
152              20                  25                  30
153  Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
154              35                  40                  45
155  Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
156      50                  55                  60
157  Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
158  65                  70                  75                  80
159  Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
160              85                  90                  95
161  Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
162             100                 105                 110
163  His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
164             115                 120                 125
165  Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
166             130                 135                 140
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```
167  Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
168  145               150               155               160
169  Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
170              165               170               175
171  Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
172              180               185               190
173  Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
174          195               200               205
175  Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
176          210               215               220
177  Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
178  225               230               235               240
179  Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
180              245               250               255
181  Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
182          260               265               270
183  Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
184          275               280               285
185  Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
186          290               295               300
187  Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
188  305               310               315               320
189  Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
190              325               330               335
191  Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
192          340               345               350
193  Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
194          355               360               365
195  Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
196          370               375               380
197  Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
198  385               390               395               400
199  Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
200              405               410               415
201  Gln Met Ser
```

VERIFICATION SUMMARY   DATE: 04/11/2002
PATENT APPLICATION: **US/10/044,622**   TIME: 09:14:19

Input Set : **N:\Crf3\RULE60\10044622.raw**
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]